In the claims:

Please amend the claims as follows:

1. (amended) A variant human MLH1 or MSH2 gene selected from the group consisting of hMLH1 mutant 1, hMSH2 mutant 1, hMSH2 mutant 2 and hMSH2 mutant 3.

2. (amended) A method of diagnosing hereditary non-polyposis colorectal cancer in a patient comprising:

(a) obtaining a DNA sample from a patient; and

(b) screening the DNA sample for the presence of a variant human MLH1 or MSH2 gene of claim 1, wherein the presence of the variant gene is indicative of hereditary non-polyposis colorectal cancer.

3. (amended) A method for predicting susceptibility of a patient to developing hereditary non-polyposis colorectal cancer comprising:

(a) obtaining a DNA sample from a patient: and

(b) screening the DNA sample for the presence of a variant human MLH1 or MSH2 gene of claim 1, wherein the presence of the variant gene is indicative of a susceptibility to hereditary non-polyposis colorectal cancer.